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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Examiner: Dr. E. Stole

Case: FJ 122

Applicant(s): Marina Vrlijc et al.

Serial No.: 09/105,117

In Response To
Paper No:

Filing Date: 17/06/98

Art Unit: 3402

Title: PROCESS FOR THE MICROBIAL PRODUCTION OF AMINO ACIDS BY BOOSTED ACTIVITY OF EXPORT CARRIERS

Hon. Commissioner of Patents and Trademarks
Washington, DC 20231

November 24, 1999

SIR:

This is in response to the Official Action dated [illegible]

A substitute computer readable form (CRF) of the "Sequence Listing" is enclosed together with a substitute paper copy of the Sequence Listing.

Please enter the substitute paper copy in the specification.

The content of the paper and computer readable copies are the same and include no new matter.

Some explanations however are presented below since in the nucleotide sequence as it was filed with the present application, the DNA sequence is present partially in a double strand representation, specifically in the range of nucleotide 900 – 960 and nucleotide 1680 to 1740.

It is quite common among the persons skilled in the art to describe a nucleotide sequence partially as a DNA double strand if it is to be made clear that, by the DNA double strand, different polypeptides are to be coded, which are not all coded by the same single strand.

In the present case, the export carrier is coded by the Gen Lys E in 5' – 3' – reading direction (from the left to the right. The likely regulator of the Lys E-genes, that is, the Lys G-gene as well as a partially open reading frame orf 3 are to be read on the respective opposite strand in the opposite direction of Lys E, that is, in the 3' – 5' – reading direction (from the right to the left).

For preparation of the required sequence protocols in PatentIn-format, two separate individual strands were prepared from the partially overlapping combination of the two individual strands with opposite reading directions, as they were represented by the originally filed 2374 bp-long nucleotide sequence. This was done in accordance with the common knowledge of a person skilled in the art.

In reality, this means that the sequence protocol designated by No. 1 (corresponding data register entry name: lys E. app) codes from the nucleotide 1016 to the nucleotide 1726 for the export carrier Lys E. The preceding and the subsequent nucleotide sequence (nt 1 – 1015 and nt1727 – 2374) was translated "literally" on the basis of the originally filed nucleotide sequence.

The sequence protocol designated by the numeral 2 (corresponding data register name: Lys G-orf 3.app) codes from nucleotide 2 to 652 for a partially open reading frame orf 3 and from nucleotide 1421 to 2293 for the likely regulator Lys G. This sequence protocol corresponds to the originally filed protocol, which was read however from the back to the front (that is, from nt2374 to 1). Correspondingly, the range of the original sequence, which codes in the original sequence for LysE and which represents herein the opposite strand, was also "literally" translated.

It is affirmed that the nucleotide sequences represented in the two sequence protocols do not include any information, which was not present in the originally filed nucleotide sequences. Both sequence protocols can be clearly retrieved from the

originally filed nucleotide sequences using the knowledge and experience of a person of average skill in the art.

Respectfully submitted,

K. Bach

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